

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:01:12 ON 16 NOV 2006

L1 2214 S ABCG2 OR BCRP  
L2 869 S INDOLOCARBAZOLE  
L3 13 S L1 AND L2  
L4 7 DUP REMOVE L3 (6 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 15:03:11 ON 16 NOV 2006

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:05:48 ON 16 NOV 2006

L5 14029 S C421A OR 421  
L6 25 S L1 AND L5  
L7 11 DUP REMOVE L6 (14 DUPLICATES REMOVED)

## EAST Search History

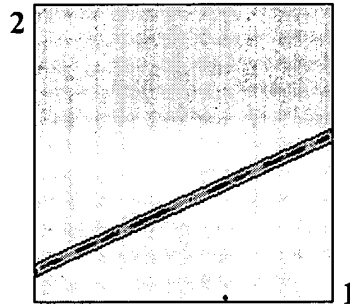
Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	197	ABCG2 or BCRP	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L2	318083	snp or mutation or polymorphism or variant	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L3	134	L1 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L4	140707	"421" or C421A	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L5	24	L1 and L2 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:58
L6	28	L1 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L7	335	indolocarbazole	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L8	4	L1 and L7 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 15:00

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ View option   
 Masking character option  Masking color option   
☐ Show CDS translation

**Sequence 1:** gi|44847528|emb|CQ757490.1|Sequence 1 from Patent WO2003107249.  
 Length = 1968 (1 .. 1968)

**Sequence 2:** gi|62526032|ref|NM\_004827.2|Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA  
 Length = 4445 (1 .. 4445)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



4445

Score = 3757 bits (1954), Expect = 0.0  
 Identities = 1968/1968 (100%), Gaps = 0/1968 (0%)  
 Strand=Plus/Plus

Query 1 *seq id #1* ATGTCTTCCAGTAATGTCTGAAGTTTTTATCCCAGTGTCTACAAGGAAACACCAATGGCTTC 60  
 Sbjct 494 ATGTCTTCCAGTAATGTCTGAAGTTTTTATCCCAGTGTCTACAAGGAAACACCAATGGCTTC 553  
 Query 61 CCCGCGACAGCTTCCAATGACCTGAAGGCATTTACTGAAGGAGCTGTGTTAAGTTTTTCAT 120  
 Sbjct 554 CCCGCGACAGCTTCCAATGACCTGAAGGCATTTACTGAAGGAGCTGTGTTAAGTTTTTCAT 613  
 Query 121 AACATCTGCTATCGAGTAAACTGAAGAGTGGCTTTCTACCTTGTCGAAAACAGTTGAG 180  
 Sbjct 614 AACATCTGCTATCGAGTAAACTGAAGAGTGGCTTTCTACCTTGTCGAAAACAGTTGAG 673  
 Query 181 AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTCAACGCCATCCTGGGA 240  
 Sbjct 674 AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTCAACGCCATCCTGGGA 733  
 Query 241 CCCACAGGTGGAGGCAAATCTTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT 300

Sbjct	734	 CCCACAGGTGGAGGCAAATCTTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT	793
Query	301	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCGACCTGCCAATTTCAAATGTAAT 	360
Sbjct	794	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCGACCTGCCAATTTCAAATGTAAT	853
Query	361	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACCTTA 	420
Sbjct	854	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACCTTA	913
Query	421	CAGTTCTCAGCAGCTCTTCGGCTTGCAACAACATGACGAATCATGnnnnnnnnCGAACGG 	480
Sbjct	914	CAGTTCTCAGCAGCTCTTCGGCTTGCAACAACATGACGAATCATGAAAAAACGAACGG	973
Query	481	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAACCT 	540
Sbjct	974	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAACCT	1033
Query	541	CAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAAGGACTAGTATAGGAATGGAGCTT 	600
Sbjct	1034	CAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAAGGACTAGTATAGGAATGGAGCTT	1093
Query	601	ATCACTGATCCTTCCATCTTGTTCTTGGATGAGCCTACAACCTGGCTTAGACTCAAGCACA 	660
Sbjct	1094	ATCACTGATCCTTCCATCTTGTTCTTGGATGAGCCTACAACCTGGCTTAGACTCAAGCACA	1153
Query	661	GCAAATGCTGTCCTTTTGCTCCTGAAAAGGATGTCTAAGCAGGGACGAACAATCATCTTC 	720
Sbjct	1154	GCAAATGCTGTCCTTTTGCTCCTGAAAAGGATGTCTAAGCAGGGACGAACAATCATCTTC	1213
Query	721	TCCATTTCATCAGCCTCGATATTCCATCTTCAAGTTGTTTGATAGCCTCACCTTATTGGCC 	780
Sbjct	1214	TCCATTTCATCAGCCTCGATATTCCATCTTCAAGTTGTTTGATAGCCTCACCTTATTGGCC	1273
Query	781	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTTGGGATACTTTGAATCAGCT 	840
Sbjct	1274	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTTGGGATACTTTGAATCAGCT	1333
Query	841	GGTTATCACTGTGAGGCCTATAATAACCCTGCAGACTTCTTCTTGGACATCATTAATGGA 	900
Sbjct	1334	GGTTATCACTGTGAGGCCTATAATAACCCTGCAGACTTCTTCTTGGACATCATTAATGGA	1393
Query	901	GATTCCACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG 	960
Sbjct	1394	GATTCCACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG	1453
Query	961	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTTATGTCAACTCCTCC 	1020
Sbjct	1454	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTTATGTCAACTCCTCC	1513
Query	1021	TTCTACAAAGAGACAAAAGCTGAATTACATCAACTTTCCGGGGGTGAGAAGAAGAAGAAG 	1080
Sbjct	1514	TTCTACAAAGAGACAAAAGCTGAATTACATCAACTTTCCGGGGGTGAGAAGAAGAAGAAG	1573
Query	1081	ATCACAGTCTTCAAGGAGATCAGCTACACCACCTCCTTCTGTTCATCAACTCAGATGGGTT 	1140
Sbjct	1574	ATCACAGTCTTCAAGGAGATCAGCTACACCACCTCCTTCTGTTCATCAACTCAGATGGGTT	1633
Query	1141	TCCAAGCGTTCATTCAAAAACCTTGCTGGGTAATCCCCAGGCCTCTATAGCTCAGATCATT 	1200
Sbjct	1634	TCCAAGCGTTCATTCAAAAACCTTGCTGGGTAATCCCCAGGCCTCTATAGCTCAGATCATT	1693
Query	1201	GTCACAGTCGTAAGTGGGACTGGTTATAGGTGCCATTTACTTTGGGCTAAAAAATGATTCT 	1260
Sbjct	1694	GTCACAGTCGTAAGTGGGACTGGTTATAGGTGCCATTTACTTTGGGCTAAAAAATGATTCT	1753

Query	1261	ACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTCCTGACGACCAACCAGTGTTCAGC	1320
Sbjct	1754	ACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTCCTGACGACCAACCAGTGTTCAGC	1813
Query	1321	AGTGTTCAGCCGTGGAACCTCTTTGTGGTAGAGAAGAAGCTCTTCATACATGAATACATC	1380
Sbjct	1814	AGTGTTCAGCCGTGGAACCTCTTTGTGGTAGAGAAGAAGCTCTTCATACATGAATACATC	1873
Query	1381	AGCGGATACTACAGAGTGTCTATCTTATTTTCCTTGGAACCTGTTATCTGATTTATTACCC	1440
Sbjct	1874	AGCGGATACTACAGAGTGTCTATCTTATTTTCCTTGGAACCTGTTATCTGATTTATTACCC	1933
Query	1441	ATGAGGATGTTACCAAGTATTATATTTACCTGTATAGTGTACTTCATGTTAGGATTGAAG	1500
Sbjct	1934	ATGAGGATGTTACCAAGTATTATATTTACCTGTATAGTGTACTTCATGTTAGGATTGAAG	1993
Query	1501	CCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACCCTTATGATGGTGGCTTATTCAGCC	1560
Sbjct	1994	CCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACCCTTATGATGGTGGCTTATTCAGCC	2053
Query	1561	AGTTCCATGGCACTGGCCATAGCAGCAGGTGAGAGTGTGGTTTCTGTAGCAACACTTCTC	1620
Sbjct	2054	AGTTCCATGGCACTGGCCATAGCAGCAGGTGAGAGTGTGGTTTCTGTAGCAACACTTCTC	2113
Query	1621	ATGACCATCTGTTTTGTGTTTATGATGATTTTTTCAGGTCTGTTGGTCAATCTCACAACC	1680
Sbjct	2114	ATGACCATCTGTTTTGTGTTTATGATGATTTTTTCAGGTCTGTTGGTCAATCTCACAACC	2173
Query	1681	ATTGCATCTTGGCTGTCATGGCTTCAGTACTTCAGCATTCCACGATATGGATTTACGGCT	1740
Sbjct	2174	ATTGCATCTTGGCTGTCATGGCTTCAGTACTTCAGCATTCCACGATATGGATTTACGGCT	2233
Query	1741	TTGCAGCATAATGAATTTTTGGGACAAAACCTTCTGCCAGGACTCAATGCAACAGGAAAC	1800
Sbjct	2234	TTGCAGCATAATGAATTTTTGGGACAAAACCTTCTGCCAGGACTCAATGCAACAGGAAAC	2293
Query	1801	AATCCTTGTAACATATGCAACATGTACTGGCGAAGAATATTTGGTAAAGCAGGGCATCGAT	1860
Sbjct	2294	AATCCTTGTAACATATGCAACATGTACTGGCGAAGAATATTTGGTAAAGCAGGGCATCGAT	2353
Query	1861	CTCTCACCTGGGGCTTGTGGAAGAATCACGTGGCCTTGGCTTGTATGATTGTTATTTTC	1920
Sbjct	2354	CTCTCACCTGGGGCTTGTGGAAGAATCACGTGGCCTTGGCTTGTATGATTGTTATTTTC	2413
Query	1921	CTCACAATTGCCTACCTGAAATTGTTATTTCTTAAAAAATATTCTTAA	1968
Sbjct	2414	CTCACAATTGCCTACCTGAAATTGTTATTTCTTAAAAAATATTCTTAA	2461

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Sequences: 1  
 Number of Hits to DB: 608  
 Number of extensions: 9  
 Number of successful extensions: 1  
 Number of sequences better than 10.0: 1

Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Length of query: 1968  
Length of database: 18,419,680,154  
Length adjustment: 27  
Effective length of query: 1941  
Effective length of database: 18,419,680,127  
Effective search space: 35752599126507  
Effective search space used: 35752599126507  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 15 (29.5 bits)  
S2: 22 (43.0 bits)